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<110>KAO CORPORATION

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<150>JP P1999-163569
<151>1999-06-10

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<213>Bacillus sp. KSM-K38

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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
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Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
              35   40   45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu

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                50                      55                      60
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
        65                      70                      75                      80
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
                        85                      90                      95
Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
                100                     105                     110
Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
                115                     120                     125
Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
                130                     135                     140
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145                     150                     155                     160
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
                        165                     170                     175
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
                        180                     185                     190
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
                        195                     200                     205
Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
                210                     215                     220
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225                     230                     235                     240
Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
                        245                     250                     255
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
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30

260   265   270
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu

          275   280   285
Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met

     290   295   300
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala

305   310   315   320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu

                   325   330   335
Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu

          340   345   350
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly

          355   360   365
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu

     370   375   380
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe

385   390   395   400
Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg

                   405   410   415
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser

          420   425   430
Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp

          435   440   445
Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp

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<213>Bacillus sp. KSM-AP1378

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                    20   25   30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
          35   40   45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
       50   55   60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65   70   75   80

Thr Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly
                    85   90   95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
                    100   105   110

Gly Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
          115   120   125

Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
       130   135   140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145   150   155   160

His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
                165   170   175

Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
                180   185   190

Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
                195   200   205

Asp His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
        210   215   220

Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225   230   235   240

Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
                245   250   255

Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
                260   265   270

Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
        275   280   285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
        290   295   300

Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305   310   315   320

His Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
                325   330   335

Gly Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala
        340   345   350

33

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355   360   365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser
        370   375   380

Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr
385   390   395   400

Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
                405   410   415

Gly Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
                420   425   430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly
        435   440   445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile
        450   455   460

Asn Ala Asp Gly Trp Gly Asn Phe Thr Val Asn Gly Gly Ala Val Ser
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Val Trp Val Lys Gln
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<213>Bacillus sp. KSM-K38

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ttatgatata tgtaagcgtt atcattaaaa ggaggtattt g atg aga aga tgg gta   176

gta gca atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca   224

gat gga ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa   272
Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu

 1   5   10   15

aac gac ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg   320
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu

            20   25   30

agt gat gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt   368
Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly

         35   40   45

aat agt cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta   416
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu

35

gga gag ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag 464
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65   70   75   80

gca cag ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat 512
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
     85   90   95

gta tac gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg 560
Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
     100   105   110

gag gca gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat 608
Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
     115   120   125

att tca ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca 656
Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
     130   135   140

ggg cgt aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt 704
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145   150   155   160

aat ggt gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc 752
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
     165   170   175

ttt gca aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat 800
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
     180   185   190

tat gat tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta 848

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Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
        195                 200                 205

caa gat gag ttg aag gat tgg ggt agc tgg ttt acc gat gag tta gat      896
Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
    210                 215                 220

ttg gat ggt tat cgt tta gat gct att aaa cat att cca ttc tgg tat      944
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225                 230                 235                 240

aca tct gat tgg gtt cgg cat cag cgc aac gaa gca gat caa gat tta      992
Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
                245                 250                 255

ttt gtc gta ggg gaa tat tgg aag gat gac gta ggt gct ctc gaa ttt     1040
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
                260                 265                 270

tat tta gat gaa atg aat tgg gag atg tct cta ttc gat gtt cca ctt     1088
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
                275                 280                 285

aat tat aat ttt tac cgg gct tca caa caa ggt gga agc tat gat atg     1136
Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
        290                 295                 300

cgt aat att tta cga gga tct tta gta gaa gcg cat ccg atg cat gca     1184
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305                 310                 315                 320

gtt acg ttt gtt gat aat cat gat act cag cca ggg gag tca tta gag     1232
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
                325                 330                 335
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37

tca tgg gtt gct gat tgg ttt aag cca ctt gct tat gcg aca att ttg   1280
Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
            340   345   350

acg cgt gaa ggt ggt tat cca aat gta ttt tac ggt gat tac tat ggg   1328
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
            355   360   365

att cct aac gat aac att tca gct aaa aaa gat atg att gat gag ctg   1376
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
            370   375   380

ctt gat gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt   1424
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385   390   395   400

gat cat tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga   1472
Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
                    405   410   415

cct aat tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc   1520
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
                420   425   430

aag tgg atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat   1568
Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
            435   440   445

tta act ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg   1616
Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
            450   455   460

ggc gaa ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa   1664

38

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465   470   475   480

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cttaacgctt ctacgacttt gaagcttta   1753

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<213>Bacillus sp. KSM-K36

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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Glu Ala Leu
                        20   25   30

Ser Asn Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
                        35   40   45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
                        50   55   60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65   70   75   80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
                        85   90   95

Val Tyr Gly Asp Val Val Met Asn His Lys Leu Gly Ala Asp Phe Thr
                        100   105   110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Ser Asn Arg Trp Gln Asp

39

115   120   125
Ile Ser Gly Val Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Pro
          130   135   140
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145   150   155   160
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Leu Phe Arg
                    165   170   175
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
                    180   185   190
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
                    195   200   205
Gln Glu Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
          210   215   220
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225   230   235   240
Thr Ser Asp Trp Val Arg His Gln Arg Ser Glu Ala Asp Gln Asp Leu
                    245   250   255
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
          260   265   270
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
          275   280   285
Asn Tyr Asn Phe Tyr Arg Ala Ser Lys Gln Gly Gly Ser Tyr Asp Met
          290   295   300
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Ile His Ala
305   310   315   320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu

40

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
            340   345   350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
        355   360   365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
    370   375   380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385   390   395   400

Asp His Trp Asp Ile Val Gly Trp Thr Arg Glu Gly Thr Ser Ser Arg
            405   410   415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
            420   425   430

Lys Trp Met Tyr Val Gly Gln Gln His Ala Gly Gln Thr Trp Thr Asp
        435   440   445

Leu Thr Gly Asn His Ala Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
    450   455   460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465   470   475   480

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gat ggc ttg aat gga acg atg atg cag tat tat gag tgg cat cta gag       150
Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
1               5                   10                  15

aat gat ggg caa cac tgg aat cgg ttg cat gat gat gcc gaa gct tta       198
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Glu Ala Leu
            20                  25                  30

agt aat gcg ggt att aca gct att tgg ata ccc cca gcc tac aaa gga      246
Ser Asn Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
        35                  40                  45

aat agt cag gct gat gtt ggg tat ggt gca tac gac ctt tat gat tta      294
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
    50                  55                  60
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42

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ggg gag ttt aat caa aaa ggt acc gtt cga acg aaa tac ggg aca aag        342
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65                  70                  75                  80

gct cag ctt gag cga gct ata ggg tcc cta aag tcg aat gat atc aat        390
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
                    85                  90                  95

gtt tat ggg gat gtc gta atg aat cat aaa tta gga gct gat ttc acg        438
Val Tyr Gly Asp Val Val Met Asn His Lys Leu Gly Ala Asp Phe Thr
                    100                 105                 110

gag gca gtg caa gct gtt caa gta aat cct tcg aac cgt tgg cag gat        486
Glu Ala Val Gln Ala Val Gln Val Asn Pro Ser Asn Arg Trp Gln Asp
                    115                 120                 125

att tca ggt gtc tac acg att gat gca tgg acg gga ttt gac ttt cca        534
Ile Ser Gly Val Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Pro
                    130                 135                 140

ggg cgc aac aat gcc tat tcc gat ttt aaa tgg aga tgg ttc cat ttt        582
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145                 150                 155                 160

aat ggc gtt gac tgg gat caa cgc tat caa gaa aac cat ctt ttt cgc        630
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Leu Phe Arg
                    165                 170                 175

ttt gca aat acg aac tgg aac tgg cga gtg gat gaa gag aat ggt aat        678
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
                    180                 185                 190

tat gac tat tta tta gga tcg aac att gac ttt agc cac cca gag gtt        726
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
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43

caa gag gaa tta aag gat tgg ggg agc tgg ttt acg gat gag cta gat   774
Gln Glu Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
        210   215   220

tta gat ggg tat cga ttg gat gct att aag cat att cca ttc tgg tat   822
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225   230   235   240

acg tca gat tgg gtt agg cat cag cga agt gaa gca gac caa gat tta   870
Thr Ser Asp Trp Val Arg His Gln Arg Ser Glu Ala Asp Gln Asp Leu
                245   250   255

ttt gtc gta ggg gag tat tgg aag gat gac gta ggt gct ctc gaa ttt   918
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
                260   265   270

tat tta gat gaa atg aat tgg gag atg tct cta ttc gat gtt ccg ctc   966
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
                275   280   285

aat tat aat ttt tac cgg gct tca aag caa ggc gga agc tat gat atg   1014
Asn Tyr Asn Phe Tyr Arg Ala Ser Lys Gln Gly Gly Ser Tyr Asp Met
        290   295   300

cgt aat att tta cga gga tct tta gta gaa gca cat ccg att cat gca   1062
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Ile His Ala
305   310   315   320

gtt acg ttt gtt gat aat cat gat act cag cca gga gag tca tta gaa   1110
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
                325   330   335

tca tgg gtc gct gat tgg ttt aag cca ctt gct tat gcg aca atc ttg   1158

44

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
            340   345   350

acg cgt gaa ggt ggt tat cca aat gta ttt tac ggt gac tac tat ggg   1206
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
            355   360   365

att cct aac gat aac att tca gct aag aag gat atg att gat gag ttg   1254
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
            370   375   380

ctt gat gca cgt caa aat tac gca tat ggc aca caa cat gac tat ttt   1302
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385   390   395   400

gat cat tgg gat atc gtt gga tgg aca aga gaa ggt aca tcc tca cgt   1350
Asp His Trp Asp Ile Val Gly Trp Thr Arg Glu Gly Thr Ser Ser Arg
                    405   410   415

cct aat tcg ggt ctt gct act att atg tcc aat ggt cct gga gga tca   1398
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
                    420   425   430

aaa tgg atg tac gta gga cag caa cat gca gga caa acg tgg aca gat   1446
Lys Trp Met Tyr Val Gly Gln Gln His Ala Gly Gln Thr Trp Thr Asp
            435   440   445

tta act ggc aat cac gcg gcg tcg gtt acg att aat ggt gat ggc tgg   1494
Leu Thr Gly Asn His Ala Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
            450   455   460

ggc gaa ttc ttt aca aat gga gga tct gta tcc gtg tat gtg aac caa   1542
Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
465   470   475   480

45

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ctcaacgctt ctacgaagct tta   1625

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agtcatccag aggtcgtaga tgagttgaag gat 33

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gttgactggg atgagcgcaa acaagaaaat cat

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